

#8
BP
9-6-01 1638RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/548,971DATE: 08/07/2001
TIME: 08:16:07Input Set : A:\19452a-7.app
Output Set: N:\CRF3\08072001\I548971.raw

RECEIVED

SEP 04 2001

TECH CENTER 1600/2900

Does Not Comply
Corrected Diskette Needed

PP-35

3 <110> APPLICANT: Liljegren, Sarah
 4 Yanofsky, Martin F.
 5 The Regents of the University of California
 7 <120> TITLE OF INVENTION: Control of Fruit Dehiscence in Arabidopsis by
 8 INDEHISCENT1 Genes
 10 <130> FILE REFERENCE: 19452A-000700US
 12 <140> CURRENT APPLICATION NUMBER: US 09/548,971
 13 <141> CURRENT FILING DATE: 2000-04-13
 15 <150> PRIOR APPLICATION NUMBER: US 60/090,649
 16 <151> PRIOR FILING DATE: 1998-06-25
 18 <150> PRIOR APPLICATION NUMBER: US 09/339,998
 19 <151> PRIOR FILING DATE: 1999-06-25
 21 <160> NUMBER OF SEQ ID NOS: 9
 23 <170> SOFTWARE: PatentIn Ver. 2.1
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 26 <211> LENGTH: 3856
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Arabidopsis thaliana
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: INDEHISCENT1 (IND1) genomic
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 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (2765)..(3361)
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 49 actggtatat tgttgatgaa tataacaagt atgaacatta atgcatgaaa cggggtattt 360
 51 tgtcttgaac tcattaaagg caatgtgaaa agaagatgtg aggtctcatt ttgaaaattt 420
 53 atcttctagc tttgtcgatt ttaaattctat gaaatgaacg caacatatag aaatttcatg 480
 55 tggacaacga ctttagacg gtatcttaatt tagaccgatt aattagtaatt atacttata 540
 57 atataattag tgggtattat aagtttactt atccacttga gaatttaaacc aatgggcaat 600
 59 accttaattg cgaaagaagc cgctcccact tcgtgtaatt agttatgggg gagagatcct 660
 61 gttaaatcgt caaataaaac aacttaagaa ctagaatttg acacaaaaaa tcataaagag 720
 63 aacgttgaa gagtcattta tcgtatccag ctcatatttc ctgactaaga tcaaatcaag 780
 65 gccgttgaaa gggcttgtaa gaaaatgtcg aagaaaccgt ggggtttaga agaaagacaa 840
 67 gaaatagaag aacaatgatg ttaaatggcc tattttggtg tataggagtt gtcaaaagag 900
 69 gagagagaga agaaaattag gtcaaaataa tgagcactaa aatggagac atgtgttgag 960
 71 taactattac aagagcgact tatgcttcct tatggcaatg atatccaaac caaagtgcaa 1020
 73 cgctcctttt ttgcccatt ttctgtaaagt ctctctcctt ctctgtcctt aggaaaaacc 1080
 75 ctagaaattt aatcccttgt tcttgatctt gctttttgag taaccatgat ttgaccaca 1140
 77 cactatttct tctattcttt gtggtctata ggtatttgct ttatatgtgt ttcttgatt 1200
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 81 aatgagtcca tgaaatttgt tagcgaaaaa ggtagaaata tattgagtct ttaaaccggca 1320

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83 atatatataa ttttctgca aaacttagct ttaatcatga tctaatagata ttttctttaa 1380
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87 cattcacaca aactaaact taattagaac tctaggaaat attttaaaat gacaacttta 1500
89 tcgaaaaaaa tttagttatg aaaacaattc cagaattaaa catgagctat ataatttaag 1560
91 ataaaatgaa gtaatatgta tatgtatgta ataacatatc tgattgcggt aaaaaaaac 1620
93 atatctgatt aaattgttca tgcaggccca tgtcactatg atgtcatcac gtttttattt 1680
95 tcacaataac taatatatat tcaaaaaaat agttttgtca gattaaattt tttttggtgg 1740
97 tcagctttct ccaacctact aaactagttt ggaatgttct cttctttatt tttcttttcc 1800
99 ttgatttctt atgtttttta ttatggaat ttaagacgg attgtttagg tcgtttctct 1860
101 cttttcttgt tttctaaagt tacttttgtt aactcatctc ctcccaatta gacagtcaat 1920
103 catatagtta tcttttaata tatgtctagt tgataaaaaa aatgaaaaaa tactggtggt 1980
105 agtttacta atgttttgtt aaaaaatctg atattatgaa tctaataaat ttctttgatc 2040
107 gtataatgtg ggttaatttt agtaattttt tacataaata agaactgtaa tgttgatgta 2100
109 tattggggaa tcagtatatg agcttgggta actatacttc tggaaatact tgaagattta 2160
111 actatttgca aaattataat ttagtcccg aaaaatacaga cgacgggaca cgacaacata 2220
113 taagcaggtt tgaatcttgg aaaattttgt atacataacc tatataaata ctaatgttct 2280
115 ggttgggttc aaaagccttt tcaaaagttc cattttttaa attcaaggac attttacata 2340
117 ggaaataagt tgagtcataa aaaataatgg ttattttgta aggttttttt tttgattaaa 2400
119 acgcacatat taagaagtta gtttttttcc actaccaaat atcaattaat ttaaaacat 2460
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127 ataataagag acatgcatgt aagcattcgg ttaattaatc gagtcaaaga tatatatcag 2700
129 taaatacata tgtgtatatt tctggaaaaa gaatatatat attgagaaat aagaaaagat 2760
131 gaaa atg gaa aat ggt atg tat aaa aag aaa gga gtg tgc gac tct tgt 2809
132 Met Glu Asn Gly Met Tyr Lys Lys Lys Gly Val Cys Asp Ser Cys
133 1 5 10 15
135 gtc tcg tcc aaa agc aga tcc aac cac agc ccc aaa aga agc atg atg 2857
136 Val Ser Ser Lys Ser Arg Ser Asn His Ser Pro Lys Arg Ser Met Met
137 20 25 30
139 gag cct cag cct cac cat ctc ctc atg gat tgg aac aaa gct aat gat 2905
140 Glu Pro Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn Asp
141 35 40 45
143 ctt ctc aca caa gaa cac gca gct ttt ctc aat gat cct cac cat ctc 2953
144 Leu Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu
145 50 55 60
147 atg tta gat cca cct ccc gaa acc cta att cac ttg gac gaa gac gaa 3001
148 Met Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu
149 65 70 75
151 gag tac gat gaa gac atg gat gcg atg aag gag atg cag tac atg atc 3049
152 Glu Tyr Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met Ile
153 80 85 90 95
155 gcc gtc atg cag ccc gta gac atc gac cct gcc acg gtc cct aag ccg 3097
156 Ala Val Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro
157 100 105 110
159 aac cgc cgt aac gta agg ata agc gac gat cct cag acg gtg gtt gct 3145
160 Asn Arg Arg Asn Val Arg Ile Ser Asp Pro Gln Thr Val Val Ala
161 115 120 125
163 cgt cgg cgt cgg gaa agg atc agc gag aag atc cga att ctc aag agg 3193

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168 Ile Val Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu
169      145      150      155
171 gcc ata cgt tac acc aag ttc ttg aaa cgg cag gtg agg att ctt cag 3289
172 Ala Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu Gln
173 160      165      170      175
175 cct cac tct cag att gga gct cct atg gct aac ccc tct tac ctt tgt 3337
176 Pro His Ser Gln Ile Gly Ala Pro Met Ala Asn Pro Ser Tyr Leu Cys
177      180      185      190
179 tat tac cac aac tcc caa ccc tga tgaactacac agaagctcgc tagctagaca 3391
180 Tyr Tyr His Asn Ser Gln Pro
181      195
183 tttggtgtca tcctctcaac ctttttcatg ttgatattat atatatagat gcataaagat 3451
185 tcgatccaag attgtatggg tgttttaata ttattattct aagatatatg atgtacaatt 3511
187 gtgtaccaag tttctttatc ttgatatcat atgcataaat aattggtgaa taaaaagaag 3571
189 atattgattg taaacaaaaa aaagaagata ttgattgtta attagggttt gatcattctg 3631
191 tatgaaagct ttggcctgca aattaatttt cgatatatat atatatatat ggagaatata 3691
193 tatcaaatat ttttttaatt tgactataat ttgtatcaat tatctgaatc tgatgagtgt 3751
195 aggttatata tggattagca aaaaagaaaa caaccattat tacgcaccta cattaaaaat 3811
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200 <210> SEQ ID NO: 2
201 <211> LENGTH: 198
202 <212> TYPE: PRT
203 <213> ORGANISM: Arabidopsis thaliana
204 <223> OTHER INFORMATION: INDEHISCENT1 (IND1) protein need field 220
206 <400> SEQUENCE: 2
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211 Pro Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn Asp Leu
212      35      40      45
213 Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu Met
214      50      55      60
215 Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu Glu
216 65      70      75      80
217 Tyr Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met Ile Ala
218      85      90      95
219 Val Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn
220      100      105      110
221 Arg Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Thr Val Val Ala Arg
222      115      120      125
223 Arg Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Ile
224      130      135      140
225 Val Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala
226 145      150      155      160
227 Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu Gln Pro

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237 <212> TYPE: DNA
238 <213> ORGANISM: Arabidopsis thaliana
240 <220> FEATURE:
241 <223> OTHER INFORMATION: 5' untranslated region IND1 promoter OK
243 <400> SEQUENCE: 3
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246 tgtaaaagaa aaaaccttat gttaatatca ccgtaggcaa aaaaaatata tcatcatatt 180
247 aaatTTTTat tataagatta tacattctct cgttgtaaga gttactccaa ttgcaagtgt 240
248 tgtattaact aataaaaagg acgaaagtag gaagcttata attaatgat gttgcatagt 300
249 actggtatat tgttgatgaa tataacaagt atgaacatta atgcatgaaa cggggtattt 360
250 tgtcttgaac tcattaaagg caatgtgaaa agaagatgtg aggtctcatt ttgaaaattt 420
251 atcttctagc tttgtcgatt ttaaatctat gaaatgaacg caacatatag aaatttcatt 480
252 tggacaacga catttagacg gtatcttaat tagaccgatt aattagtaat atacttatat 540
253 atataattag tgggtgattat aagtttactt atccacttga gaattttaaac aatgggcaat 600
254 accttaattg cgaagaagac cgtcccaact tcgtgtaatg agttatgggg gagagatcct 660
255 gttaaatcgt caaataaaac aacttaagaa ctagaaattg acacaaaaaa tcataaagag 720
256 aacgttgaag aagtcattta tcgtatccag ctcatatttc ctagctaaga tcaaatcaag 780
257 gccgttgaag gggcttgtaa gaaaatgtcg aagaaaccgt ggggtttaga agaaagacaa 840
258 gaaatagaag aacaatgatg ttaaatgcc tattttggtg tataggagtt gtcaaaagag 900
259 gagagagaga agaaaattag gtcaaaataa tgagcactaa aaatggagac atgtgttgag 960
260 taactattac aagagcgact tatgcttcct tatggcaatg atatccaaac caaagtgcac 1020
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268 cattcacaca acactaaact taattagaac tctaggaaat attttaaaat gacaacttta 1500
269 tcgaaaaaaa tttagttatg aaaacaattc cagaattaaa catgagctat ataatttaag 1560
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272 tcacaataac taatatatat tcaaaaaaat agttttgtca gattaaattt tttttggtgg 1740
273 tcagctttct ccaacctact aaactagtct ggaatgttct cttcttttatt tttcttttc 1800
274 ttgattttct atgtttttta tttatggaaat ttttaagacg attgtttagg tcgtttctct 1860
275 cttttcttgt tttctaaagt tacttttgta aactcatctc ctcccaatta gacagtcaat 1920
276 catatagtta tcttttaata tatgtctagt tgataaaaaa aatgaaaaaa tactggtggt 1980
277 agttctacta atgtttgtgt aaaaaatctg atattatgaa tctaataaat ttctttgatc 2040
278 gtataatgtg ggttaaattt agtaattttt tacataaata agaactgtaa tgttgatgta 2100
279 tattggggaa tcagtatatt agcttgggta actatacttc tggaaatact tgaagattta 2160
280 actatttgca aaattataat ttagtccoga aaaatacaga cgacggggaca cgacaacata 2220

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283 ggaaataagt tgagtcataa aaaataatgg ttatcttgta aggttttttt tttgattaaa 2400
284 acgcacatat taagaagtta gttttttttc actaccaaatt atcaattaat ttaaaacccat 2460
285 gcaaccattc ataaaacaat actattaaag aatataaata atcacaaaat attaaatata 2520
286 cttaaaatct acatataaat ttacaaaaca tctaattaat tgaaacagaa aggaaaaggt 2580
287 aaaatatatc ataaaatgag acatatatcc tataaaaaaa aaatgaggca tatgaagtaa 2640
288 ataataagag acatgcatgt aagcattcgg ttaattaatc gagtcaaaga tatatatcag 2700
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295 <212> TYPE: DNA

296 <213> ORGANISM: Arabidopsis thaliana

298 <220> FEATURE:

299 <223> OTHER INFORMATION: 3' untranslated region IND1 promoter

301 <400> SEQUENCE: 4

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304 attattattc taagatatat gatgtacaat tgtgtaccaa gtttctttat cttgatata 180
305 tatgcataaa taattggtga ataaaaagaa gatattgatt gtaaacaaaa aaaagaagat 240
306 attgattggt aattagggtt tgatcattct gtatgaaagc tttggcctgc aaattaattt 300
307 tcgatataata tatatatata tggagaatat atatcaaata cttttttaat ttgactataa 360
308 tttgtatcaa ttatctgaat ctgatgagtg taggttatat atggattagc aaaaaagaaa 420
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313 <210> SEQ ID NO: 5

314 <211> LENGTH: 5622

315 <212> TYPE: DNA

316 <213> ORGANISM: Arabidopsis thaliana

318 <220> FEATURE:

319 <223> OTHER INFORMATION: SHATTERPROOF1 (SHP1) genomic

321 <220> FEATURE:

322 <221> NAME/KEY: modified_base

323 <222> LOCATION: (935)..(941)

324 <223> OTHER INFORMATION: n = any nucleotide

326 <400> SEQUENCE: 5

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329 gattttctgta tcagtggtca tatttgtgga tccaacgtat tcatcatcaa gttctcaagt 180
330 ttgctttcag tgcaattcta attcacacgt ttaactttta catgcatgctc attataatta 240
331 cttcttcaact aagacacaat acggcaaacc ttccagatta tattaatctc cataaatgaa 300
332 ataattaacc tcataatcaa gattcaatgt ttctaaatat atatggacaa aatttacacg 360
333 gaagattaga tacgtatatt agtagattta gtctttcggt tgtgcgataa gattaaccac 420
334 ctcatagata gtaatatcat tgtcaaattc ctctcggttt agtcgctaaa ttgtatcttt 480
335 tttaagccta aaagtagtgt attcgcataat gaattatcgt cctaactttt tttttaatta 540
336 acaaaaaaat cgaaaagaaa ataactctgtt aaatattttt taagtactcc attaagttta 600
337 gtttcttatt aaaaaatgct tgaaatttga cagttatggt caacaatttt gaatcatgag 660
338 cgatgtctag atactcagaa tttaatcaag atgtcttata aaatttggtg tcactcgagg 720

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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5